ABSTRACT

Background: Diverse strains of simian immunodeficiency virus (SIV) infect over 40 species of African nonhuman primates (NHP) and continuously pose potential threat of transmission to humans. However, strain diversity amongst common free-ranging *Chlorocebus aethiops* (African green monkey-AGMs) and *Papio anubis* (Olive baboon) in Kenya remains unclear. For the first time, we investigated epidemiology and diversity of SIV in AGMs and Baboon from major Kenyan urban centres.

Methods & Materials: A total of 126 AGMs and 65 olive baboons from Mombasa, Kisumu and Naivasha were sampled once *in situ* and released. Blood samples were spotted on whatman FTA cards for DNA/RNA extraction. Total DNA from dried blood on FTA (DB-FTA) was subjected to PCR followed by high resolution melting (HRM) analysis using consensus primers targeting a 650-bp fragment in partial *pol* gene and a 900-bp fragment of *env* gene encompassing hypervariable V3–V5 regions.

Results: PCR-HRM analysis illustrated amplification of SIV fragments giving an overall infection rate of 30.95% (39/126) in AGMs and 3.07% (2/65) in Olive baboons. Subsequent sequence identification confirmed SIV infection in AGM and for the first time in olive baboon. Phylogenetic analysis of *pol* and *env* genes revealed extensive genetic diversity among newly generated SIVagm sequences within groups sympatric NHPs and within a geographical location. Signatures of pervasive and episodic diversifying selection were also detected on the *env* gene indicating continuous SIV diversification.

Conclusion: This molecular evidence of SIVagm in olive baboons illustrates continuous simian-to-simian SIV transmission in the wild and can be linked to potential risks of transmission to humans through consumption of monkey bushmeat. In addition, this study shows that DB-FTA specimens and PCR-HRM analysis can be used as a cost-effective alternative sampling method for the surveillance and monitoring of SIV and other retrovirus of public health importance.